

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: SOPPET, DANIEL R.  
RUBEN, STEVEN M.
- (ii) TITLE OF INVENTION: HEMATOPOIETIC SIGNALING FACTOR
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
  - (B) STREET: 1100 NEW YORK AVENUE, SUITE 600
  - (C) CITY: WASHINGTON
  - (D) STATE: DC
  - (E) COUNTRY: US
  - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To be assigned
  - (B) FILING DATE: Herewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/035,577
  - (B) FILING DATE: 16-JAN-1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: STEFFE, ERIC K
  - (B) REGISTRATION NUMBER: 36,688
  - (C) REFERENCE/DOCKET NUMBER: 1488.0600001
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (202) 371-2600
  - (B) TELEFAX: (202) 371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1545 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 66..1202
- (ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 144..1202

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 66..141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGGCTTCGG	GTCGGTGCAA	GGCAGGCGCA	CGGGAAAGGG	CGCGCCGCGC	GGCCGCCACC	60
CCACC	ATG CTC AAG CGC TGC GGC CGG CGC CTG CTG CTG GCG CTG GCG	Met Leu Lys Arg Cys Gly Arg Arg	Leu Leu Ala Leu Ala			107
-26	-25	-20	-15			
Gly Ala	Leu Ala Cys Leu Leu Val Leu Thr Ala Asp Pro Pro Pro					155
-10	-5	1				
CCT CCA CTG CCC GCC GAG CGC GGC CGG CGC GCG CTG CGC AGC CTG GCG	Pro Pro Leu Pro Ala Glu Arg Gly Arg Arg	Ala Leu Arg Ala	Leu Arg Ser	Leu Ala		203
5	10	15	20			
Gly Pro Ala Gly Ala Ala Pro Ala Pro	Gly Leu Gly Ala Ala Ala					251
25	30	35				
GCG CCC GCG GGG GCT GCC CCG GCG CCC GGG CTG GGG GCG GCG GCG GCG	Ala Pro Gly Ala Leu Val Arg Asp Val His Ser Leu Ser Glu Tyr Phe					299
40	45	50				
AGC CTG CTC ACC CGC GCG CGC AGA GAT GCG GGC CCG CCG CCC GGG GCT	Ser Leu Leu Thr Arg Ala Arg Asp Ala Gly Pro Pro Gly Ala					347
55	60	65				
GCC CCC CGC CCC GCC GAC GGC CAC CCG CGC CCC CTG GCC GAG CCG CTC	Ala Pro Arg Pro Ala Asp Gly His Pro Arg Pro Leu Ala Glu Pro Leu					395
70	75	80				
GCG CCC CGA GAC GTC TTC ATC GCT GTC AAG ACC ACC AAA AAG TTC CAC	Ala Pro Arg Asp Val Phe Ile Ala Val Lys Thr Thr Lys Lys Phe His					443
85	90	95	100			
CGC GCG CGC CTC GAC CTG CTG GAG ACC TGG ATC TCG CGC CAC AAG	Arg Ala Arg Leu Asp Leu Leu Glu Thr Trp Ile Ser Arg His Lys					491
105	110	115				
GAG ATG ACG TTC ATC TTC ACT GAC GGG GAA GAT GAG GCG CTG GCC AGG	Glu Met Thr Phe Ile Phe Thr Asp Gly Glu Asp Glu Ala Leu Ala Arg					539
120	125	130				
CAC ACG GGC AAC GTG GTC ATC ACA AAC TGC TCG GCC GCC CAC AGC CGC	His Thr Gly Asn Val Val Ile Thr Asn Cys Ser Ala Ala His Ser Arg					587
135	140	145				
CAG GCG CTG TCC TGC AAG ATG GCC GTG GAG TAT GAC CGC TTC ATC GAG	Gln Ala Leu Ser Cys Lys Met Ala Val Glu Tyr Asp Arg Phe Ile Glu					635
150	155	160				

TCC GGC AGG AAG TGG TTC TGC CAC GTG GAC GAT GAC AAC TAC GTC AAC	683
Ser Gly Arg Lys Trp Phe Cys His Val Asp Asp Asp Asn Tyr Val Asn	
165 170 175 180	
CTG CGG ACC CTG CTG CGA CTG CTG GCC AGC TAC CCG CAC ACG CGG GAC	731
Leu Arg Thr Leu Leu Arg Leu Leu Ala Ser Tyr Pro His Thr Arg Asp	
185 190 195	
GTC TAC GTC GGC AAG CCC AGC CTG GAC AGG CCC ATC CAG GCC ATG GAG	779
Val Tyr Val Gly Lys Pro Ser Leu Asp Arg Pro Ile Gln Ala Met Glu	
200 205 210	
CGG GTC AGC GAG AAC AAG GTG CGT CCT GTC CAC TTC TGG TTT GCC ACG	827
Arg Val Ser Glu Asn Lys Val Arg Pro Val His Phe Trp Phe Ala Thr	
215 220 225	
GGC GGC GCT GGC TTC TGC ATC AGC CGT GGG CTG GCT CTG AAG ATG AGC	875
Gly Gly Ala Gly Phe Cys Ile Ser Arg Gly Leu Ala Leu Lys Met Ser	
230 235 240	
CCG TGG GCC AGC GGG GGT CAC TTC ATG AAT ACG GCT GAG CGG ATC CGG	923
Pro Trp Ala Ser Gly Gly His Phe Met Asn Thr Ala Glu Arg Ile Arg	
245 250 255 260	
CTG CCT GAT GAC TGC ACC ATC GGC TAC ATC GTG GAG GCC CTG CTG GGT	971
Leu Pro Asp Asp Cys Thr Ile Gly Tyr Ile Val Glu Ala Leu Leu Gly	
265 270 275	
GTG CCC CTC ATC CGC AGC GGC CTC TTC CAC TCC CAC CTG GAG AAC CTG	1019
Val Pro Leu Ile Arg Ser Gly Leu Phe His Ser His Leu Glu Asn Leu	
280 285 290	
CAG CAG GTG CCC ACC TCG GAG CTC CAC GAG CAG GTG ACG CTG AGC TAC	1067
Gln Gln Val Pro Thr Ser Glu Leu His Glu Gln Val Thr Leu Ser Tyr	
295 300 305	
GGT ATG TTT GAA AAC AAG CGG AAC GCC GTC CAC GTG AAG GGG CCC TTC	1115
Gly Met Phe Glu Asn Lys Arg Asn Ala Val His Val Lys Gly Pro Phe	
310 315 320	
TCG GTG GAG GCC GAC CCA TCC AGG TTC CGC TCC ATC CAC TGC CAC CTG	1163
Ser Val Glu Ala Asp Pro Ser Arg Phe Arg Ser Ile His Cys His Leu	
325 330 335 340	
TAC CCG GAC ACA CCC TGG TGT CCC CGC ACT GCC ATC TTC TAGTGGCCAT	1212
Tyr Pro Asp Thr Pro Trp Cys Pro Arg Thr Ala Ile Phe	
345 350	
GGCTGAGACC CAATCCCTGG GCGCCCTGG TATCCAAAGG GCCCAGGGAC CCTGTTGCGC	1272
TGCCCTGGCC TCGGCATTGCA AGGCTCCCCCT AGGGCCGTGC CTGTGCGTGT GCGTGTGCGT	1332
GTGTGTGTGT GTGTACTGCA TGCCCACCCG GGTAGCAGGC TGCTGGCAG TTCTGCTCTG	1392
TGGAGGGGCG GGCACCAGCG CCACTTATGT GCCTCTGCTC CGAGGGCCAG TGGTATGGAG	1452
GGTCTGCTTG GAGGAAGGAT TTGTGTGTCG GAGGACACTC CGAGGGCAAT TCTGTTAGGA	1512
TTTGTGGATC TTTCTACAGC TACGGGGCTC CGG	1545

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 379 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Lys Arg Cys Gly Arg Arg Leu Leu Leu Ala Leu Ala Gly Ala  
-26 -25 -20 -15

Leu Leu Ala Cys Leu Leu Val Leu Thr Ala Asp Pro Pro Pro Pro Pro  
-10 -5 1 5

Leu Pro Ala Glu Arg Gly Arg Arg Ala Leu Arg Ser Leu Ala Gly Pro  
10 15 20

Ala Gly Ala Ala Pro Ala Pro Gly Leu Gly Ala Ala Ala Ala Pro  
25 30 35

Gly Ala Leu Val Arg Asp Val His Ser Leu Ser Glu Tyr Phe Ser Leu  
40 45 50

Leu Thr Arg Ala Arg Asp Ala Gly Pro Pro Pro Gly Ala Ala Pro  
55 60 65 70

Arg Pro Ala Asp Gly His Pro Arg Pro Leu Ala Glu Pro Leu Ala Pro  
75 80 85

Arg Asp Val Phe Ile Ala Val Lys Thr Thr Lys Lys Phe His Arg Ala  
90 95 100

Arg Leu Asp Leu Leu Leu Glu Thr Trp Ile Ser Arg His Lys Glu Met  
105 110 115

Thr Phe Ile Phe Thr Asp Gly Glu Asp Glu Ala Leu Ala Arg His Thr  
120 125 130

Gly Asn Val Val Ile Thr Asn Cys Ser Ala Ala His Ser Arg Gln Ala  
135 140 145 150

Leu Ser Cys Lys Met Ala Val Glu Tyr Asp Arg Phe Ile Glu Ser Gly  
155 160 165

Arg Lys Trp Phe Cys His Val Asp Asp Asp Asn Tyr Val Asn Leu Arg  
170 175 180

Thr Leu Leu Arg Leu Leu Ala Ser Tyr Pro His Thr Arg Asp Val Tyr  
185 190 195

Val Gly Lys Pro Ser Leu Asp Arg Pro Ile Gln Ala Met Glu Arg Val  
200 205 210

Ser Glu Asn Lys Val Arg Pro Val His Phe Trp Phe Ala Thr Gly Gly  
215 220 225 230

Ala Gly Phe Cys Ile Ser Arg Gly Leu Ala Leu Lys Met Ser Pro Trp  
235 240 245

Ala Ser Gly Gly His Phe Met Asn Thr Ala Glu Arg Ile Arg Leu Pro  
250 255 260

Asp Asp Cys Thr Ile Gly Tyr Ile Val Glu Ala Leu Leu Gly Val Pro  
265 270 275

Leu Ile Arg Ser Gly Leu Phe His Ser His Leu Glu Asn Leu Gln Gln  
280 285 290

Val Pro Thr Ser Glu Leu His Glu Gln Val Thr Leu Ser Tyr Gly Met  
295 300 305 310

Phe Glu Asn Lys Arg Asn Ala Val His Val Lys Gly Pro Phe Ser Val  
315 320 325

Glu Ala Asp Pro Ser Arg Phe Arg Ser Ile His Cys His Leu Tyr Pro  
330 335 340

Asp Thr Pro Trp Cys Pro Arg Thr Ala Ile Phe  
345 350

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 375 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Leu Lys Asn Trp Gly Lys Lys Leu Leu Ser Ile Val Gly Ala  
1 5 10 15

Thr Leu Thr Cys Leu Leu Val Leu Val Val Asp Gln Gln Ser Arg His  
20 25 30

Met Leu Glu Thr Gln Ser Asp His Glu Pro Gly Ser Ala Ala Ala Val  
35 40 45

His Leu Arg Ala Asp Leu Asp Pro Ala Asn Pro Gly Asp Gly Gly Asp  
50 55 60

Pro Ala Asn Ser Ala Gln Asp Ser Gly Thr Phe Ser Ala Tyr Phe Asn  
65 70 75 80

Lys Leu Thr Arg Val Arg Arg Asp Val Glu Gln Val Ala Ala Pro Ser  
85 90 95

Lys Asp Ser Ala Ala Pro Glu Glu Asp Ile Thr Ala Asn Asp Val Phe  
100 105 110

Ile Ala Val Lys Thr Thr Lys Lys Phe His Arg Ser Arg Met Asp Leu  
115 120 125

Leu Met Asp Thr Trp Ile Ser Arg Asn Lys Glu Gln Thr Phe Ile Phe  
130 135 140

Thr Asp Gly Glu Asp Glu Glu Leu Gln Lys Lys Thr Gly Asn Val Glu  
145 150 155 160

Ser Thr Asn Cys Ser Ala Ala His Ser Arg Gln Ala Leu Ser Cys Lys  
165 170 175

Met Ala Val Glu Tyr Asp Lys Phe Ile Glu Ser Asp Lys Lys Trp Phe  
180 185 190

Cys His Val Asp Asp Asp Asn Tyr Val Asn Val Arg Thr Leu Val Lys  
195 200 205

Leu Leu Ser Arg Tyr Ser His Thr Asn Asp Ile Tyr Ile Gly Lys Pro  
210 215 220

Ser Leu Asp Arg Pro Ile Gln Ala Thr Glu Arg Ile Ser Glu Ser Asn  
225 230 235 240

Met Arg Pro Val Asn Phe Trp Phe Ala Thr Gly Gly Ala Gly Phe Cys  
245 250 255

Ile Ser Arg Gly Leu Ala Leu Lys Met Ser Pro Trp Ala Ser Gly Gly  
260 265 270

His Phe Met Asn Thr Ala Glu Lys Ile Arg Leu Pro Asp Asp Cys Thr  
275 280 285

Ile Gly Tyr Ile Ile Glu Ser Val Leu Gly Val Lys Leu Ile Arg Ser  
290 295 300

Asn Leu Phe His Ser His Leu Glu Asn Leu His Gln Val Pro Gln Ser  
305 310 315 320

Glu Ile His Asn Gln Val Thr Leu Ser Tyr Gly Met Phe Glu Asn Lys  
325 330 335

Arg Asn Ala Ile Leu Met Lys Gly Ala Phe Ser Val Glu Glu Asp Pro  
340 345 350

Ser Arg Phe Arg Ser Val His Cys Leu Leu Tyr Pro Asp Thr Pro Trp  
355 360 365

Cys Pro Trp Lys Ala Ala Tyr  
370 375

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CACCGTCGAC CCGCCGCCGC CTCCACTGC 29

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGTCTAACAGCT TTGGCCATTA GAAGATGGCA GTGCGGG 37

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGTCTAGAC CGCCATCATG CTCAAAGCGCT GCGG 34

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTAATACGAC TCACTATAGG GC 22

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGTCTAGACG CGGCCGCCAC CCCACCATGC TC

32

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGGGTCTAGA CCATGGCCAC TAGAAGATG

29

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGGTCTAGA CCATGGCCAC TAAGCGTAGT CTGGGACGTC GTATGGGTAG AAGATG

56

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 418 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGTTTGCNA CGGGNGGCGC TGGCTTCTNC ATCANCCGTG GGCTGGCTCT AAAGATGAGC	60
CCGTGGGCCA GCGGGGGTNA CTTCATGAAT ACGGCTGAGC GGATCCGGCN GCCTGATGAC	120
TGCACCACATCG GCTACATCGT GGAGGCCCTG CTGGGTGTGC CCCTNATCCG CAGCGGCCTN	180
TTCCACTCCC ACCTGGAGAA CCTGCAGCAG GTGCCCACCT CGGAGCTCCA CGGAGCAGGT	240
NACGCTGAGC TTACGGTATT TTTTGAAAAA AAGCGGAAAC GCCGTTCCAC GTNAAAAGGGG	300
GCCTTTTTN GGTTGGGAGG GCCGACCCAT TCCAGGTTTC CGTTTNCATT CCANTTGCNA	360
ACTTTAACC NGGGAAAAAA CCTTGGTNTT TCCCCGAAAT TGNAATTNTT TAGGTTGG	418

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 443 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCACCGAGTG AAGGGCTGCC TGCTGAAGGC CGATTTTCTC CTTCCAGACG TTCATCTTCA	60
CTGACGGGGA AGATGAGGCC CTGGCCAGGC ACACGGGTGA GCCCTGGACT TGGGGCGGGA	120
NGGGGCCCAA GCCTCCATCC AGAGCCGAAC GCTCCCCCTC CAGTCTCCCT GCCCCTCTGG	180
GCCGAGAAGT CACCAAGGGC AGGACANGGA GGGCAGTTA CTCATGGGT TTGCTCCATG	240
CCCCGGCCCA ACACTCGGNN CCCCCAATT TCATGCAAAT GAAGCCCATT CAGCCCCCG	300
GGTTCCCTTG AGCCAAGCAG CGGCAGGAGT GGCGGTTCTG GNAAAAGTGC TGATTGGCGG	360
GGCGGGCGC CTTGAAGGGT TGGTCGGAA GTCAAAGCCA AGCCCGAGTA AGTTGGAGT	420
ANGCGCCGGC CAGTTAANAA GGG	443

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 513 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCGAGTCCG GGTGCAGGTG GCAATGGACA GAGCGGAACC TGGATGGGTC AGCTTCCACA	60
GAGAATGGTC CCTTGATGTG CACTGCGTTC CGCTTGTCTCAAACATGCC ATAGCTCAGG	120
GTCACCTGCT CATGAAGCTC GGTGGTGGGC ACCTGCTGCA GGTTCTCTAG GTGGGAGTGG	180
AAGAGGCCGC TCCGGATGAG GGGTACACCC AGCAGAGCCT CTACAATGTA GCCAATGGTG	240
CAGTCATCGG GGAGCCGGAT GCGCTCTGCC GTGCTCATGA AGTGTCCCTCC ACTGGCCCAT	300
GGGCCATCTT TAGGGCCAGC CCTCGGCTGA TGCAAGGCC AGCTCCTCCG GTGGCAAACC	360
AAAAGTGGAC AGGTCTCACT TTGTGCTCGC TGATCCGTTCTGG ATGGGCCTGT	420
CCAGGCTGGG CTTGCGATGT ACACGTCTTG GGTGTGGGAA TAGCTGGCCA GGAAGCGCAG	480
CAGCGCCCGG AAGTTGACGT AGTTGTCATC ATC	513

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGCCCCCTG GCCGAGCCGC TNCGCGCCCC GAGACGTCTT CATCGCTGTC AAGACCACCA	60
AAAAGTTCCA CCGCGCGCGC CTCGACCTGC TGCTGGAGAC CTGGATCTCG CGCCACAAGG	120
AGATGACGTT CATCTTCACT GACGGGAAG ATGAGGCCCT GGCAGGCACA CGGGCAACGT	180
GGTCATCACA AACTGCTCGG CCGCCCACAG CCGCCAGCTT GNTTCCTGCA AGATGGCCGT	240
GGAGTATGAC CGCTTCATCG AGTCCGGCAG AAGTGGTTCT GCCACGTGGA CGATGACAAC	300
TACGTCAACC TCGGGGCCCT GCTNCGGCTG CTGGCCAGCT GACCCGCACA CG	352

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACAGGTCTCA	CTTTGTGCTC	GCTGATCCGT	TCTGTGGCCT	GGATGGGCTG	TCCAGCTGGG	60
CTTGCATGT	CACGTCTTGG	GTGTGGGAT	AGCTGCCAG	GAGCCGCAGC	AGCGCCCGGA	120
GTTGACGTAG	TTGTCATCAT	CCACGTGGCA	GAACCACTTC	TTCCCAGACT	CAATGAATCG	180
GTCATACTCC	ACAGCCATCT	TGCAGGACAG	AGCCTGGCGC	TGTGGGCCGA	GGAGCAGTTG	240
GTGAGCACCA	CATTGCCTGT	GAGCTTGCC	AGAGCTTCGT	CCTCCCCATC	AGTGAAGATG	300
AACGTCATCT	CCTTGTGGCG	CGAGATCCAG	GTCTCGAACCA	GCAGATCGAG	CCGCGCGCGG	360
TGAAACTTTC	TGGTGGTCTT	GACGGCGATG	AAGACGTCGC	GAGGGACAG	AACTTTCGGC	420
GGGGGACGCG	GATGGCGTC	GCCCTGCGA				449